STRUCTURE FILE UPDATES: 3 NOV 2003 HIGHEST RN 612478-18-9
DICTIONARY FILE UPDATES: 3 NOV 2003 HIGHEST RN 612478-18-9

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http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

=> s levansucrase/cn
L1 1 LEVANSUCRASE/CN

=> d

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2003 ACS on STN
RN 9030-17-5 REGISTRY
CN Fructosyltransferase, sucrose 6- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN E.C. 2.4.1.10
CN **Levansucrase**
CN Sucrose 6-fructosyltransferase
CN Sucrose:fructan 6-fructosyltransferase
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CABA,
CAPLUS, CASREACT, CHEMCATS, EMBASE, IFICDB, IFIPAT, IFIUDB, PROMT,
TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
464 REFERENCES IN FILE CA (1907 TO DATE)
3 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
468 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> log y

| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
|---|---|---|
| FULL ESTIMATED COST | 6.70 | 7.12 |

STN INTERNATIONAL LOGOFF AT 09:26:43 ON 04 NOV 2003

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PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

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| NEWS | 1 | | Web Page URLs for STN Seminar Schedule - N. America |
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| NEWS | 3 | SEP 09 | CA/CAplus records now contain indexing from 1907 to the present |
| NEWS | 4 | AUG 05 | New pricing for EUROPATFULL and PCTFULL effective August 1, 2003 |
| NEWS | 5 | AUG 13 | Field Availability (/FA) field enhanced in BEILSTEIN |
| NEWS | 6 | AUG 18 | Data available for download as a PDF in RDISCLOSURE |
| NEWS | 7 | AUG 18 | Simultaneous left and right truncation added to PASCAL |
| NEWS | 8 | AUG 18 | FROSTI and KOSMET enhanced with Simultaneous Left and Righ Truncation |
| NEWS | 9 | AUG 18 | Simultaneous left and right truncation added to ANABSTR |
| NEWS | 10 | SEP 22 | DIPPR file reloaded |
| NEWS | 11 | SEP 25 | INPADOC: Legal Status data to be reloaded |
| NEWS | 12 | SEP 29 | DISSABS now available on STN |
| NEWS | 13 | OCT 10 | PCTFULL: Two new display fields added |
| NEWS | 14 | OCT 21 | BIOSIS file reloaded and enhanced |
| NEWS | 15 | OCT 28 | BIOSIS file segment of TOXCENTER reloaded and enhanced |

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|---|---|
| NEWS EXPRESS | OCTOBER 01 CURRENT WINDOWS VERSION IS V6.01a, CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP), AND CURRENT DISCOVER FILE IS DATED 23 SEPTEMBER 2003 |
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| FULL ESTIMATED COST | 0.42 | 0.42 |

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**STN SEARCH** **09/986,682**

**11/4/03**

```
=> s fructosyl (2w) transferase or fructofuranosidase
L1        1008 FILE MEDLINE
L2        1965 FILE CAPLUS
L3         369 FILE SCISEARCH
L4         571 FILE LIFESCI
L5         467 FILE BIOSIS
L6        1358 FILE EMBASE

TOTAL FOR ALL FILES
L7        5738 FRUCTOSYL (2W) TRANSFERASE OR FRUCTOFURANOSIDASE

=> s l7 and (gene or nucleic acid or cdna or dna or rna)


TOTAL FOR ALL FILES
L14       1231 L7 AND (GENE OR NUCLEIC ACID OR CDNA OR DNA OR RNA)

=> s l14 and bacillus
TOTAL FOR ALL FILES
L21         63 L14 AND BACILLUS

=> s l21 not 1997-2003/py
TOTAL FOR ALL FILES
L28         37 L21 NOT 1997-2003/PY

=> dup rem l28
PROCESSING COMPLETED FOR L28
L29          26 DUP REM L28 (11 DUPLICATES REMOVED)

=> d ibib abs 1-26

L29  ANSWER 1 OF 26  SCISEARCH  COPYRIGHT 2003 THOMSON ISI on STN
ACCESSION NUMBER:    96:877923  SCISEARCH
THE GENUINE ARTICLE: VU295
TITLE:               Purification and characterization of 1-SST, the key enzyme
                     initiating fructan biosynthesis in young chicory roots
                     (Cichorium intybus)
AUTHOR:              VandenEnde W; VanWonterghem D; Dewil E; Verhaert P; DeLoof
                     A; VanLaere A (Reprint)
CORPORATE SOURCE:    KATHOLIEKE UNIV LEUVEN, INST BOT, DEPT BIOL, KARDINAAL
                     MERCIERLAAN 92, B-3001 HEVERLEE, BELGIUM (Reprint);
                     KATHOLIEKE UNIV LEUVEN, INST BOT, DEPT BIOL, B-3001
                     HEVERLEE, BELGIUM; DEPT ANIM SCI, B-3001 HEVERLEE,
                     BELGIUM; INST ZOOL, LAB DEV PHYSIOL & MOLEC BIOL, B-3000
                     LOUVAIN, BELGIUM
COUNTRY OF AUTHOR:   BELGIUM
SOURCE:              PHYSIOLOGIA PLANTARUM, (NOV 1996) Vol. 98, No. 3, pp.
                     455-466.
                     Publisher: MUNKSGAARD INT PUBL LTD, 35 NORRE SOGADE, PO
                     BOX 2148, DK-1016 COPENHAGEN, DENMARK.
                     ISSN: 0031-9317.
DOCUMENT TYPE:       Article; Journal
FILE SEGMENT:        LIFE; AGRI
LANGUAGE:            English
REFERENCE COUNT:     55
                    *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
```

AB A genuine 1-SST (sucrose:sucrose 1-**fructosyl transferase**, EC 2.4.1.99) was purified and characterized from young chicory roots (Cichorium intybus L. var. foliosum cv. Flash) by a combination of ammonium sulfate precipitation, concanavalin A affinity chromatography, anion and cation exchange chromatography. This protocol produced a 63-fold purification and a specific activity of 4.75 U (mg protein)(-1). The mass of the enzyme was 69 kDa as estimated by gel filtration. On SDS-PAGE apparent molecular masses of 49 kDa (alpha-subunit) and 24 kDa (beta-subunit) were found. Further specification was obtained by MALDI-TOF MS detecting molecular ions at m/z 40 109 and 19 896. These two fragments were also found on a western blot using an SDS-boiled chicory root extract and chicken-raised polyclonal antibodies against the purified 1-SST, indicating that the enzyme is a

heterodimer in vivo. The N-terminus of chicory root 1-SST alpha-subunit was shown to be highly homologous with the **cDNA**-derived amino acid sequences from barley 6-SFT and a number of beta-fructosyl hydrolases (invertases and fructan hydrolases). However, chicory root 1-SST properties could be clearly differentiated from those of chicory root 1-FFT (EC 2.4.1.100), chicory root acid invertase (EC 3.2.1.26) and yeast invertase. The enzyme mainly produced 1-kestose and glucose from physiologically relevant sucrose concentrations, indicating that this 1-SST is the key enzyme initiating fructan biosynthesis in vivo. However, like chicory root 1-FFT and barley 6-SFT, the enzyme also showed some beta-**fructofuranosidase** activity (fructosyl transfer to water) at very low sucrose concentrations. Although sucrose clearly is the best substrate for the enzyme, some transferase and beta-**fructofuranosidase** activity were also detected using 1-kestose as the sole substrate.

L29 ANSWER 2 OF 26 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
ACCESSION NUMBER: 96:155227 SCISEARCH
THE GENUINE ARTICLE: TW383
TITLE: CLONING AND SEQUENCE-ANALYSIS OF THE INVERTASE **GENE** INV1 FROM THE YEAST PICHIA-ANOMALA
AUTHOR: PEREZ J A (Reprint); RODRIGUEZ J; RODRIGUEZ L; RUIZ T
CORPORATE SOURCE: UNIV LA LAGUNA, FAC FARM, DEPT MICROBIOL & BIOL CELULAR, E-38071 LA LAGUNA, SPAIN (Reprint)
COUNTRY OF AUTHOR: SPAIN
SOURCE: CURRENT GENETICS, (FEB 1996) Vol. 29, No. 3, pp. 234-240. ISSN: 0172-8083.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 39

*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB A genomic library from the yeast Pichia anomala has been constructed and employed to clone the **gene** encoding the sucrose-hydrolysing enzyme invertase by complementation of a sucrose non-fermenting mutant of Saccharomyces cerevisiae. The cloned **gene**, INV1, was sequenced and found to encode a polypeptide of 550 amino acids which contained a 22 amino-acid signal sequence and ten potential glycosylation sites, The amino-acid sequence shows significant identity with other yeast invertases and also with Kluyveromyces marxianus inulinase, a yeast beta-**fructofuranosidase** which has a different substrate specificity. The nucleotide sequences of the 5' and 3' non-coding regions were found to contain several consensus motifs probably involved in the initiation and termination of **gene** transcription.

L29 ANSWER 3 OF 26 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 95351500 EMBASE
DOCUMENT NUMBER: 1995351500
TITLE: PAM.beta.1 resolvase has an atypical recombination site and requires a histone-like protein HU.
AUTHOR: Petit M.-A.; Ehrlich D.; Janniere L.
CORPORATE SOURCE: Laboratoire de Genetique Microbienne, INRA,78352 Jouy en Josas Cedex, France
SOURCE: Molecular Microbiology, (1995) 18/2 (271-282). ISSN: 0950-382X CODEN: MOMIEE
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The broad-host-range plasmid pAM.beta.1 from Gram-positive bacteria encodes a resolvase, designated Res.beta., which shares homology with the proteins of the resolvase-invertase family. Here we report the purification and in vitro characterization of Res.beta.. This resolvase is particular in two aspects: it has an atypical binding site and requires a cofactor to promote resolution in vitro. Res.beta. binds to two regions within its resolution site res. One contains two inverted repeats (R1 and R2), the other contains only one repeat (R3). The cofactor required for resolution in vitro is present in crude extracts of both **Bacillus** subtilis and Escherichia coil and can be substituted by the a. coli

histone-like protein HU. The possible mode of action of HU in the resolution process is discussed.

L29 ANSWER 4 OF 26 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 95135701 EMBASE
DOCUMENT NUMBER: 1995135701
TITLE: Molecular cloning and characterization of the extracellular sucrase **gene** (sacC) of Zymomonas mobilis.
AUTHOR: Kannan R.; Mukundan G.; Ait-Abdelkader N.; Augier-Magro V.; Baratti J.; Gunasekaran P.
CORPORATE SOURCE: Departement de Chimie, 163, avenue de Luminy,F-13288 Marseille Cedex 9, France
SOURCE: Archives of Microbiology, (1995) 163/3 (195-204). ISSN: 0302-8933 CODEN: AMICCW
COUNTRY: Germany
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The Zymomonas mobilis **gene** sacC that en codes the extracellular sucrase (protein B46) was cloned and expressed in Escherichia coli. The **gene** was found to be present downstream to the already described levansucrase **gene** sacB in the cloned chromosomal fragment of Z. mobilis. The expression product was different from SacB and exhibited sucrase but not levansucrase activity; therefore, SacC behaves like a true sucrase. Expression of sacC in E. coli JM109 and XL1 was very low; overexpression was observed in E. coli BL21 after induction of the T7 polymerase expression system with IPTG. Subcellular fractionation of the E. coli clone carrying plasmid pLSS2811 showed that more than 70% of the sucrase activity could be detected in the cytoplasmic fraction, suggesting that the enzyme was soluble and not secreted in E. coli. The nucleotide sequence analysis of sacC revealed an open reading frame 1239bp long coding for a 413 amino acid protein with a molecular mass of 46kDa. The first 30 deduced amino acids from this ORF were identical with those from the N-terminal sequence of the extracellular sucrase (protein B46) purified from Z. mobilis ZM4. No leader peptide sequence could be identified in the sacC **gene**. The amino acid sequence of SacC showed very little similarity to those of other known sucrases, but was very similar to the levansucrases of Z. mobilis (61.5%), Erwinia amylovora (40.2%) and **Bacillus** subtilis (25.6%).

L29 ANSWER 5 OF 26 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
ACCESSION NUMBER: 95:350193 SCISEARCH
THE GENUINE ARTICLE: QX917
TITLE: PURIFICATION AND CHARACTERIZATION OF CYCLOINULOOLIGOSACCHARIDE FRUCTANOTRANSFERASE (CFTASE) FROM **BACILLUS**-CIRCULANS MCI-2554
AUTHOR: KUSHIBE S (Reprint); MITSUI K; YAMAGISHI M; YAMADA K; MORIMOTO Y
CORPORATE SOURCE: MITSUBISHI CHEM CO, YOKOHAMA RES CTR, DIV RES & DEV, BIOSCI LAB, AOBA KU, 1000 KAMOSHIDA, YOKOHAMA, KANAGAWA 227, JAPAN (Reprint)
COUNTRY OF AUTHOR: JAPAN
SOURCE: BIOSCIENCE BIOTECHNOLOGY AND BIOCHEMISTRY, (JAN 1995) Vol. 59, No. 1, pp. 31-34. ISSN: 0916-8451.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; AGRI
LANGUAGE: ENGLISH
REFERENCE COUNT: 27
*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
AB Cycloinulooligosaccharide fructanotransferase (CFTase) that produces cyclofructan from inulin was purified about 69-fold from a culture broth of **Bacillus** circulans MCI-2554 by column chromatographies on DEAE-Toyopearl, QAE-Toyopearl, hydroxyapatite, and phenyl-Sepharose. The molecular mass of the enzyme was estimated to be 115 kDa by SDS-polyacrylamide gel electrophoresis and gel filtration, indicating a monomer structure. Maximal activity was observed at pH 7.5 and 45 degrees C. The enzyme was active from pH 5.5 to pH 9.5, and at temperatures up to 45 degrees C. The enzyme activity was inhibited by Fe2+ and Cu2+. A part

of the amino acid sequence was identical with that of beta-**fructofuranosidases** of Zymomonas mobilis, carrot, Salmonella typhimurium, and mung bean.

L29 ANSWER 6 OF 26 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 93259952 MEDLINE
DOCUMENT NUMBER: 93259952 PubMed ID: 8491724
TITLE: Molecular characterization of a fructanase produced by Bacteroides fragilis BF-1.
AUTHOR: Blatch G L; Woods D R
CORPORATE SOURCE: Department of Microbiology, University of Cape Town, Rondebosch, South Africa.
SOURCE: JOURNAL OF BACTERIOLOGY, (1993 May) 175 (10) 3058-66. Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M83774
ENTRY MONTH: 199306
ENTRY DATE: Entered STN: 19930625
Last Updated on STN: 19930625
Entered Medline: 19930611

AB The Bacteroides fragilis BF-1 fructanase-encoding **gene** (fruA) was cloned and expressed in Escherichia coli from the recombinant plasmid pBS100. The fruA **gene** consisted of 1,866 bp encoding a protein of 622 amino acids with a calculated M(r) of 70,286. The apparent M(r) of the fructanase, determined by in vitro cell-free transcription-translation and sodium dodecyl sulfate-polyacrylamide gel electrophoresis analysis, was approximately 71,500. An alignment of the amino acid sequences of the B. fragilis BF-1 fructanase and the **Bacillus** subtilis levanase revealed that 45.5% of the amino acids were identical. The fruA **gene** was expressed in E. coli from its own promoter; however, no E. coli promoter-like sequence was evident upstream from the **gene** . A major E. coli transcription start point and a single B. fragilis BF-1 transcription start point were located. Expression of the fruA **gene** was constitutive in E. coli(pBS100) and B. fragilis BF-1. The ratio of sucrase activity to inulinase activity (S/I ratio) was constant for enzyme preparations from E. coli (pBS100), indicating that both activities were associated with the fructanase. For B. fragilis BF-1, the S/I ratio varied considerably depending on the carbon source used for growth, suggesting that a separate sucrase is produced in addition to the fructanase in B. fragilis BF-1. Localization experiments and TnphoA mutagenesis indicated that the fructanase was exported to the periplasm. Sequence analysis of the N-terminal region of the fructanase revealed a putative 30-amino-acid signal peptide. The enzymatic properties of the purified fructanase were investigated.(ABSTRACT TRUNCATED AT 250 WORDS)

L29 ANSWER 7 OF 26 MEDLINE on STN
ACCESSION NUMBER: 93273516 MEDLINE
DOCUMENT NUMBER: 93273516 PubMed ID: 8500898
TITLE: Sequence analysis of scrA and scrB from Streptococcus sobrinus 6715.
AUTHOR: Chen Y Y; Lee L N; LeBlanc D J
CORPORATE SOURCE: Department of Microbiology, University of Texas Health Science Center at San Antonio 78284-7758.
CONTRACT NUMBER: DE08915 (NIDCR)
SOURCE: INFECTION AND IMMUNITY, (1993 Jun) 61 (6) 2602-10. Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L06791; GENBANK-L06792
ENTRY MONTH: 199306
ENTRY DATE: Entered STN: 19930716
Last Updated on STN: 20000303
Entered Medline: 19930628

AB The complete nucleotide sequences of Streptococcus sobrinus 6715 scrA and scrB, which encode sucrose-specific enzyme II of the phosphoenolpyruvate-

dependent phosphotransferase system and sucrose-6-phosphate hydrolase, respectively, have been determined. These two **genes** were transcribed divergently, and the initiation codons of the two open reading frames were 192 bp apart. The transcriptional initiation sites were determined by primer extension analysis, and the putative promoter regions of these two **genes** overlapped partially. The **gene** encoding enzyme IIScr, scrA, contained 1,896 nucleotides, and the molecular mass of the predicted protein was 66,529 Da. The hydropathy plot of the predicted amino acid sequence indicated that enzyme IIScr was a relatively hydrophobic protein. The **gene** encoding sucrose-6-phosphate hydrolase, scrB, contained 1,437 nucleotides. The molecular mass of the predicted protein was 54,501 Da, and the encoded enzyme was hydrophilic. The predicted amino acid sequences of the two open reading frames exhibited approximately 45 and 70% identity with those encoded by scrA and scrB, respectively, from Streptococcus mutans GS5. Homology also was observed between the N-terminal region of the S. sobrinus 6715 enzyme IIScr and other enzyme IIs specific for the glucopyranoside molecule, all of which generate glucopyranoside-6-phosphate during translocation and phosphorylation of the respective substrates. The sequence of the C-terminal domain of the S. sobrinus 6715 enzyme IIScr shared significant homology with enzyme IIIGlc from Escherichia coli and Salmonella typhimurium and with the C-terminal domain of enzyme IIBgl from E. coli, indicating that the two functional domains, enzyme IIScr and enzyme IIIScr, were covalently linked as a single polypeptide in S. sobrinus 6715. The deduced amino acid sequence of the **gene** product of S. sobrinus scrB shared strong homology with sucrase from **Bacillus** subtilis, Klebsiella pneumoniae, and Vibrio alginolyticus, suggesting conservation based on the physiological roles of these proteins.

L29 ANSWER 8 OF 26 MEDLINE on STN
ACCESSION NUMBER: 94122441 MEDLINE
DOCUMENT NUMBER: 94122441 PubMed ID: 7764362
TITLE: Expression of an 87-kD-beta-1,3-glucanase of **Bacillus** circulans IAM1165 in Saccharomyces cerevisiae by low-temperature incubation.
AUTHOR: Nakajima H; Noguchi K; Yamamoto M; Aono R; Horikoshi K
CORPORATE SOURCE: Department of Bioengineering, Tokyo Institute of Technology, Yokohama, Japan.
SOURCE: BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, (1993 Dec) 57 (12) 2039-42.
Journal code: 9205717. ISSN: 0916-8451.
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Biotechnology
ENTRY MONTH: 199403
ENTRY DATE: Entered STN: 19950809
Last Updated on STN: 19970203
Entered Medline: 19940301

AB A **DNA** segment encoding a signal peptide from yeast invertase was fused in frame to bglH **gene** encoding 87-kD-beta-1,3-glucanase from **Bacillus** circulans IAM1165 and was expressed in the yeast Saccharomyces cerevisiae under the control of the GAL1 **gene** promoter. Yeast cells containing this fused **gene** produced active beta-1,3-glucanase in the medium after a long period of incubation at low temperature. The enzyme produced by yeast was heterogeneous in size, and larger than the enzyme produced by Escherichia coli.

L29 ANSWER 9 OF 26 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 94184225 MEDLINE
DOCUMENT NUMBER: 94184225 PubMed ID: 7511014
TITLE: Molecular cloning and physiological analysis of an invertase isoenzyme in Helianthus tissues.
AUTHOR: Venuat B; Goupil P; Ledoigt G
CORPORATE SOURCE: Physiologie et Genetique vegetales, Universite Blaise Pascal (Clermont-Ferrand II), France.
SOURCE: BIOCHEMISTRY AND MOLECULAR BIOLOGY INTERNATIONAL, (1993 Dec) 31 (5) 955-66.
Journal code: 9306673. ISSN: 1039-9712.
PUB. COUNTRY: Australia

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199404
ENTRY DATE: Entered STN: 19940509
Last Updated on STN: 19960129
Entered Medline: 19940422

AB A soluble acid invertase activity isolated from Helianthus tuberosus (Jerusalem artichoke) shoots and analyzed by immunochromatography using polyclonal yeast antibodies, represents around 5% of the total invertase activity. This invertase isoenzyme was also isolated from dormant tuber parenchyma. In these partially dormant tissues, the specific activity of this isoenzyme is low suggesting a partial inactivation of the invertase molecules. Polyacrylamide gel electrophoresis of immunopurified fractions yields similar levels of the 58 kDa polypeptide both in shoots and dormant tubers, but with much lower activity of the enzyme in the tubers. A **cDNA** library was constructed in pUEX 1 from poly (A)+ **RNA** extracted from Jerusalem artichoke tubers. This library was screened for invertase using (i) a **Bacillus** subtilis invertase **DNA** probe and (ii) anti-yeast invertase antibodies. A recombinant clone of approximately 1.8 kb size was selected by these two methods. Using Northern blots, a temporal sequence in the expression of invertase **gene** was observed during the breaking of dormancy with the main level after 8 weeks of cold treatment at 4 degrees C. A 2.5 kb transcript was detected, translation of which would yield a 97 kDa polypeptide representing the precursor of Jerusalem artichoke invertase.

L29 ANSWER 10 OF 26 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 93078334 EMBASE
DOCUMENT NUMBER: 1993078334
TITLE: Expression of **Bacillus** subtilis neutral protease **gene** (nprE) in Saccharomyces cerevisiae.
AUTHOR: Wang L.-F.; Devenish R.J.
CORPORATE SOURCE: Department of Biochemistry, Centre Molecular Biology Medicine, Monash University,Clayton, Vic. 3168, Australia
SOURCE: Journal of General Microbiology, (1993) 139/2 (343-347). ISSN: 0022-1287 CODEN: JGMIAN
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Expression in the yeast Saccharomyces cerevisiae of the intact nprE **gene** of **Bacillus** subtilis, which encodes the pre-pro-NprE neutral protease precursor, resulted in intracellular accumulation of unprocessed precursor without detectable secretion or processing of the expressed **gene** product. When sequences specifying the signal peptide of yeast invertase were fused upstream of sequences encoding the mature NprE enzyme, nprE **gene** products were secreted into the culture medium. The secreted protein products were, however, highly glycosylated and biologically inactive.

L29 ANSWER 11 OF 26 MEDLINE on STN
ACCESSION NUMBER: 93372638 MEDLINE
DOCUMENT NUMBER: 93372638 PubMed ID: 8364409
TITLE: Duplication of secretion signal sequences is deleterious for the secretion of human interferon alpha 4 from Saccharomyces cerevisiae and **Bacillus** subtilis.
AUTHOR: Galanis M; Wang L; Nagley P; Devenish R J
CORPORATE SOURCE: Department of Biochemistry, Monash University, Clayton, Victoria, Australia.
SOURCE: BIOCHEMISTRY AND MOLECULAR BIOLOGY INTERNATIONAL, (1993 Jun) 30 (2) 271-82. Journal code: 9306673. ISSN: 1039-9712.
PUB. COUNTRY: Australia
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199310

ENTRY DATE: Entered STN: 19931022
Last Updated on STN: 20000303
Entered Medline: 19931001

AB Tandem duplication of a mitochondrial import leader sequence has been shown to markedly increase the efficiency of translocation of chimaeric precursors across mitochondrial membranes to the mitochondrial matrix. The principle of leader sequence duplication was applied to the protein secretion system of the yeast Saccharomyces cerevisiae and of **Bacillus** subtilis. The secretion signal sequences of yeast invertase and B. subtilis neutral protease were used to direct the secretion of human interferon alpha 4. Our results show that the duplication of these N-terminal signal sequences does not enhance secretion of interferon alpha 4 in either of the cell systems studied.

L29 ANSWER 12 OF 26 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 91291345 MEDLINE
DOCUMENT NUMBER: 91291345 PubMed ID: 1368686
TITLE: Cloning, sequencing, and characterization of the intracellular invertase **gene** from Zymomonas mobilis.
AUTHOR: Yanase H; Fukushi H; Ueda N; Maeda Y; Toyoda A; Tonomura K
CORPORATE SOURCE: Department of Biotechnology, Faculty of Engineering, Tottori University, Japan.
SOURCE: AGRICULTURAL AND BIOLOGICAL CHEMISTRY, (1991 May) 55 (5) 1383-90.
Journal code: 0370452. ISSN: 0002-1369.
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Biotechnology
ENTRY MONTH: 199108
ENTRY DATE: Entered STN: 19950809
Last Updated on STN: 19950809
Entered Medline: 19910812

AB The structural **gene** for the intracellular invertase E1 of Zymomonas mobilis strain Z6C was cloned in a 2.25-kb **DNA** fragment on pUSH11, and expressed in Escherichia coli HB101. The enzyme produced by the E. coli carrying pUSH11 was purified about 1,122 fold to homogenicity with a yield of 4%. The molecular weight and substrate specificity of the enzyme were identical with those of the intracellular invertase E1 from Z. mobilis. The nucleotides of the cloned **DNA** were sequenced; they included an open reading frame of 1,536 bp, coding for a protein with a molecular weight of 58,728. The N-terminal amino acid sequence predicted was identical with the sequence of the first 20 N-terminal amino acid residues of the protein obtained by Edman degradation. Comparison of the predicted amino acid sequence of E1 protein with those of the four other known beta-D-**fructofuranosidases** from Escherichia coli, **Bacillus** subtilis, and Saccharomyces cerevisiae indicated a stronger homology in the N-terminal portion than in the C-terminal portion.

L29 ANSWER 13 OF 26 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
ACCESSION NUMBER: 91:322158 SCISEARCH
THE GENUINE ARTICLE: FN869
TITLE: CLONING, SEQUENCING, AND CHARACTERIZATION OF THE INTRACELLULAR INVERTASE **GENE** FROM ZYMOMONAS-MOBILIS
AUTHOR: YANASE H (Reprint); FUKUSHI H; UEDA N; MAEDA Y; TOYODA A; TONOMURA K
CORPORATE SOURCE: TOTTORI UNIV, FAC ENGN, DEPT BIOTECHNOL, TOTTORI 680, JAPAN (Reprint); UNIV OSAKA PREFECTURE, FAC AGR, DEPT AGR CHEM, SAKAI, OSAKA 591, JAPAN; FUKUYAMA UNIV, FAC ENGN, DEPT FOOD TECHNOL, FUKUYAMA 72902, JAPAN
COUNTRY OF AUTHOR: JAPAN
SOURCE: AGRICULTURAL AND BIOLOGICAL CHEMISTRY, (1991) Vol. 55, No. 5, pp. 1383-1390.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; AGRI
LANGUAGE: ENGLISH
REFERENCE COUNT: 21
*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB The structural **gene** for the intracellular invertase E1 of Zymomonas mobilis strain Z6C was cloned in a 2.25-kb **DNA** fragment on pUSH11, and expressed in Escherichia coli HB101. The enzyme produced by the E. coli carrying pUSH11 was purified about 1,122 fold to homogeneity with a yield of 4%. The molecular weight and substrate specificity of the enzyme were identical with those of the intracellular invertase E1 from Z. mobilis. The nucleotides of the cloned **DNA** were sequenced; they included an open reading frame of 1,536 bp, coding for a protein with a molecular weight of 58,728. The N-terminal amino acid sequence predicted was identical with the sequence of the first 20 N-terminal amino acid residues of the protein obtained by Edman degradation. Comparison of the predicted amino acid sequence of E1 protein with those of the four other known beta-D-**fructofuranosidases** from Escherichia coli, **Bacillus** subtilis, and Saccharomyces cerevisiae indicated a stronger homology in the N-terminal portion than in the C-terminal portion.

L29 ANSWER 14 OF 26 LIFESCI COPYRIGHT 2003 CSA on STN
ACCESSION NUMBER: 91:76258 LIFESCI
TITLE: Positive and negative regulation controlling expression of the sac **genes** in **Bacillus** subtilis .
THE **BACILLUS** SUBTILIS GENOME.
AUTHOR: Debarbouille, M.; Martin-Verstraete, I.; Arnaud, M.; Klier, A.; Rapoport, G.
CORPORATE SOURCE: Unite Biochim. Microb., URA 1300, Cent. Natl. Rech. Sci., Inst. Pasteur, Dep. Biotechnol., 75724 Paris Cedex 15, France
SOURCE: RES. MICROBIOL., (1991) pp. 757-764.
Meeting Info.: International Conference on the Bacillus subtilis Genome. Paris (France). 2-5 Sep 1990.
DOCUMENT TYPE: Book
TREATMENT CODE: Conference
FILE SEGMENT: J; N; G
LANGUAGE: English
AB Two saccharolytic enzymes, sucrase (sacA **gene** product) and levansucrase (sacB **gene** product), can be detected in crude extracts of **Bacillus** subtilis after induction by sucrose. Sucrase is an intracellular enzyme, whereas levansucrase is secreted. Both enzymes are beta **-D-fructofuranosidases**, and levansucrase also catalyses the synthesis of high molecular weight fructose polymers called levan. Another **gene**, sacP, seems to form an operon with sacA. Specific and pleiotropic regulatory mechanisms affect the expression of the sucrose system in B. subtilis . Recent results dealing with specific regulation within the sac system are presented in this review.

L29 ANSWER 15 OF 26 MEDLINE on STN
ACCESSION NUMBER: 91072217 MEDLINE
DOCUMENT NUMBER: 91072217 PubMed ID: 2254250
TITLE: Cloning and sequencing of the sacA **gene**: characterization of a sucrase from Zymomonas mobilis.
AUTHOR: Gunasekaran P; Karunakaran T; Cami B; Mukundan A G; Preziosi L; Baratti J
CORPORATE SOURCE: Laboratoire de Chimie Bacterienne, Centre National de la Recherche Scientifique, Marseille, France.
SOURCE: JOURNAL OF BACTERIOLOGY, (1990 Dec) 172 (12) 6727-35.
Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M62718
ENTRY MONTH: 199101
ENTRY DATE: Entered STN: 19910308
Last Updated on STN: 19910308
Entered Medline: 19910124
AB The Zymomonas mobilis **gene** (sacA) encoding a protein with sucrase activity has been cloned in Escherichia coli and its nucleotide sequence has been determined. Potential ribosome-binding site and promoter sequences were identified in the region upstream of the **gene** which were homologous to E. coli and Z. mobilis consensus sequences. Extracts from E. coli cells, containing the sacA **gene**

, displayed a sucrose-hydrolyzing activity. However, no transfructosylation activity (exchange reaction or levan formation) could be detected. This sucrase activity was different from that observed with the purified extracellular protein B46 from Z. mobilis. These two proteins showed different electrophoretic mobilities and molecular masses and shared no immunological similarity. Thus, the product of sacA (a polypeptide of 58.4-kDa molecular mass) is a new sucrase from Z. mobilis. The amino acid sequence, deduced from the nucleotide sequence of sacA, showed strong homologies with the sucrases from **Bacillus** subtilis, Salmonella typhimurium, and Vibrio alginolyticus.

L29 ANSWER 16 OF 26 MEDLINE on STN
ACCESSION NUMBER: 88284916 MEDLINE
DOCUMENT NUMBER: 88284916 PubMed ID: 3397182
TITLE: Sequence analysis of the Streptococcus mutans scrB **gene**.
AUTHOR: Sato Y; Kuramitsu H K
CORPORATE SOURCE: Department of Microbiology-Immunology, Northwestern University Medical-Dental Schools, Chicago, Illinois 60611.
CONTRACT NUMBER: DE-03258 (NIDCR)
SOURCE: INFECTION AND IMMUNITY, (1988 Aug) 56 (8) 1956-60. Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198808
ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 20000303
Entered Medline: 19880831

AB The complete nucleotide sequence of the Streptococcus mutans GS-5 scrB **gene** coding for sucrose-6-phosphate hydrolase activity was determined. A potential ribosome-binding site as well as promoter sequences were identified upstream from the **gene**. The deduced amino acid sequence of the enzyme suggested a molecular weight of 51,750, which is similar to that estimated for the enzyme isolated from strain GS-5. The enzyme is slightly acidic, with a pI of 5.9, and is a relatively hydrophilic protein. The nucleotide and amino acid sequences of the enzyme showed significant homology with those of the sacA protein from **Bacillus** subtilis. In addition, a region of amino acid homology with the S. mutans fructosyltransferase and B. subtilis levansucrase proteins was also detected.

L29 ANSWER 17 OF 26 MEDLINE on STN
ACCESSION NUMBER: 87279919 MEDLINE
DOCUMENT NUMBER: 87279919 PubMed ID: 3112128
TITLE: Isolation of **DNA** encoding sucrase **genes** from Streptococcus salivarius and partial characterization of the enzymes expressed in Escherichia coli.
AUTHOR: Houck C M; Pear J R; Elliott R; Perchorowicz J T
SOURCE: JOURNAL OF BACTERIOLOGY, (1987 Aug) 169 (8) 3679-84. Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198709
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19980206
Entered Medline: 19870901

AB Restriction enzyme fragments containing two sucrase **genes** have been isolated from a cosmid library of Streptococcus salivarius **DNA**. The **genes** were expressed in Escherichia coli cells, and the properties of both enzymes were studied in partially purified protein extracts from E. coli. One **gene** encoding an invertase-type sucrase was subcloned on a 2.4-kilobase-pair fragment. The sucrase enzyme had a Km for sucrose of 48 mM and a pH optimum of 6.5. The S. salivarius sucrase clone showed no detectable hybridization to a yeast invertase clone. Two overlapping subclones which had 1 kilobase pair of **DNA** in common were used to localize a fructosyltransferase **gene**. The fructosyltransferase had a Km of 93 mM and a pH optimum

of 7.0. The product of the fructosyltransferase was a levan. A fructosyltransferase clone from **Bacillus** subtilis did not hybridize to S. salivarius **DNA**. The properties of the enzymes were compared with those of previously characterized sucrases.

L29 ANSWER 18 OF 26 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 87286401 MEDLINE
DOCUMENT NUMBER: 87286401 PubMed ID: 3112519
TITLE: Characterization of the levanase **gene** of **Bacillus** subtilis which shows homology to yeast invertase.
AUTHOR: Martin I; Debarbouille M; Ferrari E; Klier A; Rapoport G
SOURCE: MOLECULAR AND GENERAL GENETICS, (1987 Jun) 208 (1-2) 177-84.
Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY, WEST: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X05649
ENTRY MONTH: 198709
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19900305
Entered Medline: 19870924

AB The structural **gene** for the enzyme levanase of **Bacillus** subtilis (SacC) was cloned in Escherichia coli. The cloned **gene** was mapped by PBS1 transduction near the sacL locus on the B. subtilis chromosome, between leuA and aroD. Expression of the enzyme was demonstrated both in B. subtilis and in E. coli. The presence of sacC allowed E. coli to grow on sucrose as the sole carbon source. The complete nucleotide sequence of sacC was determined. It includes an open reading frame of 2,031 bp, coding for a protein with calculated molecular weight of 75,866 Da, including a putative signal peptide similar to precursors of secreted proteins found in **Bacilli**. The apparent molecular weight of purified levanase is 73 kDa. The sacC **gene** product was characterized in an in vitro system and in a minicell-producing strain of E. coli, confirming the existence of a precursor form of levanase of about 75 kDa. Comparison of the predicted aminoacid sequence of levanase with those of the two other known beta-D-**fructofuranosidases** of B. subtilis indicated a homology with sucrase, but not with levansucrase. A stronger homology was detected with the N-terminal region of yeast invertase, suggesting the existence of a common ancestor.

L29 ANSWER 19 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1987:61928 CAPLUS
DOCUMENT NUMBER: 106:61928
TITLE: Nucleotide sequence of the sucrase **gene** of **Bacillus** subtilis
AUTHOR(S): Fouet, Agnes; Klier, Andre; Rapoport, Georges
CORPORATE SOURCE: Dep. Biotechnol., Inst. Pasteur, Paris, 75724, Fr.
SOURCE: Gene (1986), 45(2), 221-5
CODEN: GENED6; ISSN: 0378-1119
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The sucrase [9001-57-4]**gene** (sacA) and part of the sacP locus, which corresponds to a membrane component of the phosphotransferase system (PTS) of sucrose transport of B. subtilis, were previously cloned on a 2.1-kb EcoRI **DNA** fragment. **Genes** sacA and sacP were localized on this **DNA** fragment and the nucleotide sequence of the 2.1-kb **DNA** fragment was detd. A 1440-base-pair open reading frame (480 codons) was identified coding for a deduced polypeptide of 54,827 mol. wt. which corresponds to that of purified sucrase. The amino acid sequence shares homol. with that of yeast invertase (SUC2 **gene** product). The sacA **gene** and the preceding sacP **gene** seem to belong to the same operon.

L29 ANSWER 20 OF 26 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 83005834 EMBASE
DOCUMENT NUMBER: 1983005834

TITLE: Cloning and expression in Escherichia coli of the sucrase **gene** from **Bacillus** subtilis.
AUTHOR: Fouet A.; Klier A.; Rapoport G.
CORPORATE SOURCE: Lab. Biochim. Microb., Inst. Pasteur, F-75724 Paris Cedex 15, France
SOURCE: Molecular and General Genetics, (1982) 186/3 (399-404). CODEN: MGGEAE
COUNTRY: Germany
DOCUMENT TYPE: Journal
FILE SEGMENT: 004 Microbiology
LANGUAGE: English

L29 ANSWER 21 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1977:418603 CAPLUS
DOCUMENT NUMBER: 87:18603
TITLE: Presence of a third sucrose hydrolyzing enzyme in **Bacillus** subtilis: constitutive levanase synthesis by mutants of **Bacillus** subtilis Marburg 168
AUTHOR(S): Kunst, Frank; Steinmetz, Michel; Lepesant, Jean Antoine; Dedonder, Raymond
CORPORATE SOURCE: Inst. Rech. Biol. Mol., Univ. Paris VII, Paris, Fr.
SOURCE: Biochimie (1977), 59(3), 287-92 CODEN: BICMBE; ISSN: 0300-9084
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A .beta.-D-**fructofuranosidase**, levanase, hydrolyzing sucrose, inulin, and levans was identified in B. subtilis. This enzyme cannot be detected in strain 168. However, sacL mutations, mapped on the chromosome of strain 168 between the pheA and aroD ref. markers, lead to constitutive levanase synthesis. The synthesis is repressed by C sources such as glucose, glycerol, or sucrose.

L29 ANSWER 22 OF 26 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 76006620 EMBASE
DOCUMENT NUMBER: 1976006620
TITLE: Identification of the structural **gene** for sucrase in **Bacillus** subtilis Marburg.
AUTHOR: Lepesant J.A.; Billault A.; Kejzlarova Lepesant J.; et al.
CORPORATE SOURCE: Unite Biochim. Cell., Inst. Biol. Molec., CNRS, Paris, France
SOURCE: Biochimie, (1974) 56/11-12 (1465-1470). CODEN: BICMBE
DOCUMENT TYPE: Journal
FILE SEGMENT: 022 Human Genetics
004 Microbiology
LANGUAGE: English

L29 ANSWER 23 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1971:506518 CAPLUS
DOCUMENT NUMBER: 75:106518
TITLE: **Gene** expression during outgrowth of **Bacillus** subtilis spores. Relation between **gene** order on the chromosome and temporal sequence of enzyme synthesis
AUTHOR(S): Kennett, R. H.; Sueoka, Noboru
CORPORATE SOURCE: Dep. Biochem. Sci., Princeton Univ., Princeton, NJ, USA
SOURCE: Journal of Molecular Biology (1971), 60(1), 31-44 CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English
AB During outgrowth of B. subtilis W23 spores in a defined medium, the activities of 5 enzymes studied (sucrase, trehalase, ornithine transcarbamylase, asparate transcarbamylase and threonine dehydratase) appear in a sequential manner. With 1 exception (ornithine transcarbamylase), before **DNA** synthesis begins, the enzyme activities appear in the order in which the corresponding genetic loci have been located on the genetic map. Ornithine transcarbamylase activity does not appear in the 1st round, but in the 2nd series of increases in

enzyme activity after **DNA** synthesis commences. Moreover, the appearance of this enzyme activity occurs at a time that would be expected from its relative position on the genetic map.

L29 ANSWER 24 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1965:474221 CAPLUS
DOCUMENT NUMBER: 63:74221
ORIGINAL REFERENCE NO.: 63:13733b-c
TITLE: Sequence of enzyme synthesis and **gene** replication during the cell cycle of **Bacillus** subtilis
AUTHOR(S): Masters, Millicent; Pardee, Arthur B.
CORPORATE SOURCE: Princeton Univ., Princeton, NJ
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1965), 54(1), 64-70
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The half-doubling time in the autogenous synthesis of histidase, ornithine and aspartate carbamoyl transferases, and dehydroquinase was detd. during the cell cycle of B. subtilis. This information plus the measured potential for sucrase synthesis was used to order the 5 enzyme syntheses in a linear sequence as a function of the cell division cycle. Mutants unable to produce the enzymes were mapped genetically. The sequence of enzyme syntheses corresponded well, but not exactly, to the order of the resp. genetic markers on the genome. Relative sucrase-transforming activity changed periodically during the cell cycle at approx. the same time as the potential for sucrase synthesis.

L29 ANSWER 25 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1964:77234 CAPLUS
DOCUMENT NUMBER: 60:77234
ORIGINAL REFERENCE NO.: 60:13614a-c
TITLE: Enzyme synthesis in synchronous culture of bacteria
AUTHOR(S): Masters, Millicent; Kuempel, Peter L.; Pardee, Arthur B.
CORPORATE SOURCE: Princeton Univ., Princeton, NJ
SOURCE: Biochemical and Biophysical Research Communications (1964), 15(1), 38-42
CODEN: BBRCA9; ISSN: 0006-291X
DOCUMENT TYPE: Journal
LANGUAGE: Unavailable
AB Synchrony of cell division and enzyme formation in synchronously dividing cultures was studied. A synchronous culture of Escherichia coli K12 Hfr CS101 showed a division synchrony of the cells and a stepwise increase in the rate of aspartic carbamoyltransferase (I) synthesis. In a synchronous culture of **Bacillus** subtilis the ability of the culture to produce sucrase (II) doubled once during each division cycle and the time of doubling occurred at approx. the same time during each cycle. In a synchronously growing culture the activities of I and of histidine (III)- and II-inducibility increased in a stepwise manner, with their times of doubling falling at different times in the cell cycle. When the midpoints of the enzyme and cell doubling times were plotted on a linear time scale, III increased about 10 min. before cell division, while I increased about 15 and II about 50 min. after division. A tentative explanation suggested that the enzyme-doubling times occur soon after the corresponding **gene** is replicated and indicated that enzyme studies might be used independently to map **genes**.

L29 ANSWER 26 OF 26 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1964:32900 CAPLUS
DOCUMENT NUMBER: 60:32900
ORIGINAL REFERENCE NO.: 60:5904g-h
TITLE: Identity of the sucrase of **Bacillus** subtilis Marburg with the levansucrase of B. subtilis var nigra
AUTHOR(S): Jozon-Toulouse, Edith; Dedonder, Raymond
CORPORATE SOURCE: Inst. Pasteur, Paris
SOURCE: Compt. Rend. (1963), 257(5), 1184-7
DOCUMENT TYPE: Journal
LANGUAGE: Unavailable
AB cf. CA 57, 3908d. A strain of B. subtilis var. nigra produces a sucrose

.fwdarw. levan-.beta.-fructofuranosyl transferase and levan accumulates in the medium on incubation of B. subtilis var. nigra with sucrose. Strains of B. subtilis Marburg split sucrose without apparent formation of levan. The sucrase produced by B. subtilis was prepd. by sonic disruption of the cells in 0.01M phosphate buffer, removal of the cell debris by centrifugation and pptn. with 70-100% satd. (NH4)2SO4. The **nucleic acids** were removed with 0.25M MgCl2 and the enzyme purified by chromatography on a column of hydroxylapatite and eluted with a gradiant of 0.1-2.0M phosphate buffer (pH 6.0). The fraction eluted between 0.5 and 0.8M was identical with the enzyme prepd. from B. subtilis vat. nigra; it produced levan as the nigra var. Its affinity const. is 5.4 .times. 10-2M for sucrose while 5.0 .+-. 10-2M was found for purified levansucrase from B. subtilis var nigra. Both enzymes need the addn. of starter levans of low mol. wt. Immunological identity of both enzymes was proven with the Ouchterlony method and other procedures. The amt. of enzyme produced by B. subtilis is only 7% of thai produced by the nigra var.

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=> file reg
=> s fructosyltransferase/cn
L30           1 FRUCTOSYLTRANSFERASE/CN

=> d

L30  ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2003 ACS on STN
RN   9031-67-8  REGISTRY
CN   Fructosyltransferase (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   Enzymes, fructose-transferring
CN   Fructose-transferring enzyme
CN   Fructose-transferring enzymes
CN   FTase
CN   Transfructosidase
CN   Transfructosylase
MF   Unspecified
CI   MAN
LC   STN Files:   ADISNEWS, AGRICOLA, BIOBUSINESS, BIOSIS, BIOTECHNO, CA,
       CAPLUS, CASREACT, CIN, EMBASE, PROMT, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE
             251 REFERENCES IN FILE CA (1907 TO DATE)
               1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
             254 REFERENCES IN FILE CAPLUS (1907 TO DATE)


=> s fructofuranosidase/cn
L31           0 FRUCTOFURANOSIDASE/CN

=> log y
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